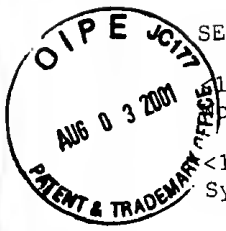

SEQUENCE LISTING

<110> Subramaniam, S.; Slater, S.; Karberg, K.; Chen, R.; Valentin, H.; Fong, Y.

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Arg Asn Asn Leu Val Arg Pro Asp Gly Gln Gly Ser Ser Leu Leu Leu

50 55 60

Tyr Pro Lys His Lys Ser Arg Phe Arg Val Asn Ala Thr Ala Gly Gln
65 70 75 80

Pro Glu Ala Phe Asp Ser Asn Ser Lys Gln Lys Ser Phe Arg Asp Ser
85 90 95

Leu Asp Ala Phe Tyr Arg Phe Ser Arg Pro His Thr Val Ile Gly Thr
100 105 110

Val Leu Ser Ile Leu Ser Val Ser Phe Leu Ala Val Glu Lys Val Ser
115 120 125

Asp Ile Ser Pro Leu Leu Phe Thr Gly Ile Leu Glu Ala Val Val Ala
130 135 140

Ala Leu Met Met Asn Ile Tyr Ile Val Gly Leu Asn Gln Leu Ser Asp
145 150 155 160

Val Glu Ile Asp Lys Val Asn Lys Pro Tyr Leu Pro Leu Ala Ser Gly
165 170 175

Glu Tyr Ser Val Asn Thr Gly Ile Ala Ile Val Ala Ser Phe Ser Ile
180 185 190

Met Ser Phe Trp Leu Gly Trp Ile Val Gly Ser Trp Pro Leu Phe Trp
195 200 205

Ala Leu Phe Val Ser Phe Met Leu Gly Thr Ala Tyr Ser Ile Asn Leu
210 215 220

Pro Leu Leu Arg Trp Lys Arg Phe Ala Leu Val Ala Ala Met Cys Ile
225 230 235 240

Leu Ala Val Arg Ala Ile Ile Val Gln Ile Ala Phe Tyr Leu His Ile
245 250 255

Gln Thr His Val Phe Gly Arg Pro Ile Leu Phe Thr Arg Pro Leu Ile
260 265 270

Phe Ala Thr Ala Phe Met Ser Phe Phe Ser Val Val Ile Ala Leu Phe
275 280 285

Lys Asp Ile Pro Asp Ile Glu Gly Asp Lys Ile Phe Gly Ile Arg Ser
290 295 300

Phe Ser Val Thr Leu Gly Gln Lys Arg Val Phe Trp Thr Cys Val Thr
305 310 315 320

Leu Leu Gln Met Ala Tyr Ala Val Ala Ile Leu Val Gly Ala Thr Ser
325 330 335

Pro Phe Ile Trp Ser Lys Val Ile Ser Val Val Gly His Val Ile Leu
340 345 350

Ala Thr Thr Leu Trp Ala Arg Ala Lys Ser Val Asp Leu Ser Ser Lys
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35 40 45

Thr Lys Cys Tyr Pro Ser Trp Asn Asp Asn Tyr Gln Val Trp Ser Lys
50 55 60

Gly Arg Glu Leu His Gln Glu Lys Phe Phe Gly Val Gly Trp Asn Tyr
65 70 75 80

Arg Leu Ile Cys Gly Met Ser Ser Ser Ser Ser Val Leu Glu Gly Lys
85 90 95

Pro Lys Lys Asp Asp Lys Glu Lys Ser Asp Gly Val Val Val Lys Lys

100 105 110

Ala Ser Trp Ile Asp Leu Tyr Leu Pro Glu Glu Val Arg Gly Tyr Ala
115 120 125

Lys Leu Ala Arg Leu Asp Lys Pro Ile Gly Thr Trp Leu Leu Ala Trp
130 135 140

Pro Cys Met Trp Ser Ile Ala Leu Ala Ala Asp Pro Gly Ser Leu Pro
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Ser Phe Lys Tyr Met Ala Leu Phe Gly Cys Gly Ala Leu Leu Leu Arg
165 170 175

Gly Ala Gly Cys Thr Ile Asn Asp Leu Leu Asp Gln Asp Ile Asp Thr
180 185 190

Lys Val Asp Arg Thr Lys Leu Arg Pro Ile Ala Ser Gly Leu Leu Thr
195 200 205

Pro Phe Gln Gly Ile Gly Phe Leu Gly Leu Gln Leu Leu Leu Gly Leu
210 215 220

Gly Ile Leu Leu Gln Leu Asn Asn Tyr Ser Arg Val Leu Gly Ala Ser
225 230 235 240

Ser Leu Leu Leu Val Phe Ser Tyr Pro Leu Met Lys Arg Phe Thr Phe
245 250 255

Trp Pro Gln Ala Phe Leu Gly Leu Thr Ile Asn Trp Gly Ala Leu Leu
260 265 270

Gly Trp Thr Ala Val Lys Gly Ser Ile Ala Pro Ser Ile Val Leu Pro
275 280 285

Leu Tyr Leu Ser Gly Val Cys Trp Thr Leu Val Tyr Asp Thr Ile Tyr
290 295 300

Ala His Gln Asp Lys Glu Asp Asp Val Lys Val Gly Val Lys Ser Thr
305 310 315 320

Ala Leu Arg Phe Gly Asp Asn Thr Lys Leu Trp Leu Thr Gly Phe Gly
325 330 335

Thr Ala Ser Ile Gly Phe Leu Ala Leu Ser Gly Phe Ser Ala Asp Leu
340 345 350

Gly Trp Gln Tyr Tyr Ala Ser Leu Ala Ala Ala Ser Gly Gln Leu Gly
355 360 365

Trp Gln Ile Gly Thr Ala Asp Leu Ser Ser Gly Ala Asp Cys Ser Arg
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35 40 45

Ala Lys Leu Gly Ile Thr Gly Val Arg Ser Asp Ala Asn Arg Val Phe
50 55 60

Ala Thr Ala Thr Ala Ala Ala Thr Ala Thr Ala Thr Thr Gly Glu Ile
65 70 75 80

Ser Ser Arg Val Ala Ala Leu Ala Gly Leu Gly His His Tyr Ala Arg
85 90 95

Cys Tyr Trp Glu Leu Ser Lys Ala Lys Leu Ser Met Leu Val Val Ala
100 105 110

Thr Ser Gly Thr Gly Tyr Ile Leu Gly Thr Gly Asn Ala Ala Ile Ser
115 120 125

Phe Pro Gly Leu Cys Tyr Thr Cys Ala Gly Thr Met Met Ile Ala Ala
130 135 140

Ser Ala Asn Ser Leu Asn Gln Ile Phe Glu Ile Ser Asn Asp Ser Lys
145 150 155 160

Met Lys Arg Thr Met Leu Arg Pro Leu Pro Ser Gly Arg Ile Ser Val
165 170 175

Pro His Ala Val Ala Trp Ala Thr Ile Ala Gly Ala Ser Gly Ala Cys
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Leu Leu Ala Ser Lys Thr Asn Met Leu Ala Ala Gly Leu Ala Ser Ala
195 200 205

Asn Leu Val Leu Tyr Ala Phe Val Tyr Thr Pro Leu Lys Gln Leu His
210 215 220

Pro Ile Asn Thr Trp Val Gly Ala Val Val Gly Ala Ile Pro Pro Leu
225 230 235 240

Leu Gly Trp Ala Ala Ala Ser Gly Gln Ile Ser Tyr Asn Ser Met Ile
245 250 255

Leu Pro Ala Ala Leu Tyr Phe Trp Gln Ile Pro His Phe Met Ala Leu
260 265 270

Ala His Leu Cys Arg Asn Asp Tyr Ala Ala Gly Gly Tyr Lys Met Leu
275 280 285

Ser Leu Phe Asp Pro Ser Gly Lys Arg Ile Ala Ala Val Ala Leu Arg
290 295 300

Asn Cys Phe Tyr Met Ile Pro Leu Gly Phe Ile Ala Tyr Asp Trp Gly
305 310 315 320

Leu Thr Ser Ser Trp Phe Cys Leu Glu Ser Thr Leu Leu Thr Leu Ala
325 330 335

Ile Ala Ala Thr Ala Phe Ser Phe Tyr Arg Asp Arg Thr Met His Lys
340 345 350

Ala Arg Lys Met Phe His Ala Ser Leu Leu Phe Leu Pro Val Phe Met
355 360 365

Ser Gly Leu Leu Leu His Arg Val Ser Asn Asp Asn Gln Gln Gln Leu
370 375 380

Val Glu Glu Ala Gly Leu Thr Asn Ser Val Ser Gly Glu Val Lys Thr
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35 40 45

Glu Ser Thr Asp Ile Val Thr Ser Glu Leu Arg Val Arg Gln Arg Gly
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Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu Leu His Asp
65 70 75 80

Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly Val Gly Ser Leu Asn

85 90 95

Val Val Met Gly Asn Lys Val Val Ala Leu Leu Ala Thr Ala Val Glu
100 105 110

His Leu Val Thr Gly Glu Thr Met Glu Ile Thr Ser Ser Thr Glu Gln
115 120 125

Arg Tyr Ser Met Asp Tyr Tyr Met Gln Lys Thr Tyr Tyr Lys Thr Ala
130 135 140

Ser Leu Ile Ser Asn Ser Cys Lys Ala Val Ala Val Leu Thr Gly Gln
145 150 155 160

Thr Ala Glu Val Ala Val Leu Ala Phe Glu Tyr Gly Arg Asn Leu Gly
165 170 175

Leu Ala Phe Gln Leu Ile Asp Asp Ile Leu Asp Phe Thr Gly Thr Ser
180 185 190

Ala Ser Leu Gly Lys Gly Ser Leu Ser Asp Ile Arg His Gly Val Ile
195 200 205

Thr Ala Pro Ile Leu Phe Ala Met Glu Glu Phe Pro Gln Leu Arg Glu
210 215 220

Val Val Asp Gln Val Glu Lys Asp Pro Arg Asn Val Asp Ile Ala Leu
225 230 235 240

Glu Tyr Leu Gly Lys Ser Lys Gly Ile Gln Arg Ala Arg Glu Leu Ala
245 250 255

Met Glu His Ala Asn Leu Ala Ala Ala Ala Ile Gly Ser Leu Pro Glu
260 265 270

Thr Asp Asn Glu Asp Val Lys Arg Ser Arg Arg Ala Leu Ile Asp Leu
275 280 285

Thr His Arg Val Ile Thr Arg Asn Lys
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35 40 45

Glu Ser Thr Asp Ile Val Thr Ser Glu Leu Arg Val Arg Gln Arg Gly
50 55 60

Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu Leu His Asp
65 70 75 80

Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly Val Gly Ser Leu Asn
85 90 95

Val Val Met Gly Asn Lys Met Ser Val Leu Ala Gly Asp Phe Leu Leu
100 105 110

Ser Arg Ala Cys Gly Ala Leu Ala Ala Leu Lys Asn Thr Glu Val Val
115 120 125

Ala Leu Leu Ala Thr Ala Val Glu His Leu Val Thr Gly Glu Thr Met
130 135 140

Glu Ile Thr Ser Ser Thr Glu Gln Arg Tyr Ser Met Asp Tyr Tyr Met

145 150 155 160

Gln Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile Ser Asn Ser Cys Lys
165 170 175

Ala Val Ala Val Leu Thr Gly Gln Thr Ala Glu Val Ala Val Leu Ala
180 185 190

Phe Glu Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Leu Ile Asp Asp
195 200 205

Ile Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu Gly Lys Gly Ser Leu
210 215 220

Ser Asp Ile Arg His Gly Val Ile Thr Ala Pro Ile Leu Phe Ala Met
225 230 235 240

Glu Glu Phe Pro Gln Leu Arg Glu Val Val Asp Gln Val Glu Lys Asp
245 250 255

Pro Arg Asn Val Asp Ile Ala Leu Glu Tyr Leu Gly Lys Ser Lys Gly
260 265 270

Ile Gln Arg Ala Arg Glu Leu Ala Met Glu His Ala Asn Leu Ala Ala
275 280 285

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Ser Arg Arg Ala Leu Ile Asp Leu Thr His Arg Val Ile Thr Arg Asn
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catgttttca ggtgatcaaa gactttgcaa gcggagagat aaagcaggcg tccagcttat 360
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tggatttcac tcagtcgaca gagcagctcg ggaagccagc agggagtgat ttggctaaag 600
gtaacttaac agcacctgtg attttcgctc tggagaggga gccaaggcta agagagatca 660
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gtgggggat taagagagca c 741

<210> 15
<211> 1087
<212> DNA
<213> Arabidopsis sp.

<400> 15

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gaaggctcag agataatgct gaactagtgt tgaaccaatt tttgctcaaa caaggtatat 540
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cctctgg 1087

<210> 16
<211> 1164
<212> DNA
<213> Arabidopsis sp.

<400> 16

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ggtttctcga cgttgatcta cgaatcaccc gggcggagat ttgttgtgcg tgcggcggag 180
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gctgcttcag ggaactttca ttggacccca gaggatgttg ctaagtcgat tctttgcatg 420
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gatatcgacg caattaatga gccatatcgt ccaattccat ctggagcaat atcagagcca 540
gaggttatta cacaagtctg ggtgctatta ttgggaggtc ttggtattgc tggaatatta 600

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gatgtgtggg cagggcatac cactcccact gtcttctatc ttgctttggg aggatcattg  660
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tttgcacttg gagcaagcta tattagtttg ccatggtggg ctggccaagc attgtttggc  780
actcttacgc cagatgttgt tgttctaaca ctcttgtaca gcatagctgg gttaggaata  840
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<210> 17
<211> 387
<212> PRT
<213> Arabidopsis sp.

<400> 17

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Thr Ser Val Asp Arg Val Gly Val Leu Ser Leu Arg Asn Ser Asp Ser
            20                  25                  30

Val Glu Phe Thr Arg Arg Arg Ser Gly Phe Ser Thr Leu Ile Tyr Glu
        35                  40                  45

Ser Pro Gly Arg Arg Phe Val Val Arg Ala Ala Glu Thr Asp Thr Asp
    50                  55                  60

Lys Val Lys Ser Gln Thr Pro Asp Lys Ala Pro Ala Gly Gly Ser Ser
65                  70                  75                  80

Ile Asn Gln Leu Leu Gly Ile Lys Gly Ala Ser Gln Glu Thr Asn Lys
                85                  90                  95

Trp Lys Ile Arg Leu Gln Leu Thr Lys Pro Val Thr Trp Pro Pro Leu
            100                 105                 110

Val Trp Gly Val Val Cys Gly Ala Ala Ala Ser Gly Asn Phe His Trp
        115                 120                 125

Thr Pro Glu Asp Val Ala Lys Ser Ile Leu Cys Met Met Met Ser Gly
    130                 135                 140

Pro Cys Leu Thr Gly Tyr Thr Gln Thr Ile Asn Asp Trp Tyr Asp Arg
145                 150                 155                 160

Asp Ile Asp Ala Ile Asn Glu Pro Tyr Arg Pro Ile Pro Ser Gly Ala
                165                 170                 175

Ile Ser Glu Pro Glu Val Ile Thr Gln Val Trp Val Leu Leu Leu Gly
            180                 185                 190

Gly Leu Gly Ile Ala Gly Ile Leu Asp Val Trp Ala Gly His Thr Thr
        195                 200                 205

Pro Thr Val Phe Tyr Leu Ala Leu Gly Gly Ser Leu Leu Ser Tyr Ile
    210                 215                 220
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Tyr Ser Ala Pro Pro Leu Lys Leu Lys Gln Asn Gly Trp Val Gly Asn
225 230 235 240

Phe Ala Leu Gly Ala Ser Tyr Ile Ser Leu Pro Trp Trp Ala Gly Gln
245 250 255

Ala Leu Phe Gly Thr Leu Thr Pro Asp Val Val Val Leu Thr Leu Leu
260 265 270

Tyr Ser Ile Ala Gly Leu Gly Ile Ala Ile Val Asn Asp Phe Lys Ser
275 280 285

Val Glu Gly Asp Arg Ala Leu Gly Leu Gln Ser Leu Pro Val Ala Phe
290 295 300

Gly Thr Glu Thr Ala Lys Trp Ile Cys Val Gly Ala Ile Asp Ile Thr
305 310 315 320

Gln Leu Ser Val Ala Gly Tyr Leu Leu Ala Ser Gly Lys Pro Tyr Tyr
325 330 335

Ala Leu Ala Leu Val Ala Leu Ile Ile Pro Gln Ile Val Phe Gln Phe
340 345 350

Lys Tyr Phe Leu Lys Asp Pro Val Lys Tyr Asp Val Lys Tyr Gln Ala
355 360 365

Ser Ala Gln Pro Phe Leu Val Leu Gly Ile Phe Val Thr Ala Leu Ala
370 375 380

Ser Gln His
385

<210> 18
<211> 981
<212> DNA
<213> Arabidopsis sp.

<400> 18

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gggtcgttga acttcgatct gaggacgtat tggacgactc tgatcaccga gatcaaccag 180
aagctggatg aggccatacc ggtcaagcac cctgcgggga tctacgaggc tatgagatac 240
tctgtactcg cacaaggcgc caagcgtgcc cctcctgtga tgtgtgtggc ggcctgcgag 300
ctcttcggtg gcgatcgcct cgccgctttc cccaccgcct gtgccctaga aatggtgcac 360
gcggcttcgt tgatacacga cgacctcccc tgtatggacg acgatcctgt gcgcagagga 420
aagccatcta accacactgt ctacggctct ggcatggcca ttctcgccgg tgacgccctc 480
ttcccactcg ccttccagca cattgtctcc cacacgcctc ctgaccttgt tccccgagcc 540
accatcctca gactcatcac tgagattgcc cgcactgtcg gctccactgg tatggctgca 600
ggccagtacg tcgaccttga aggaggtccc tttcctcttt cctttgttca ggagaagaaa 660
ttcggagcca tgggtgaatg ctctgccgtg tgcggtggcc tattgggcgg tgccactgag 720
gatgagctcc agagtctccg aaggtacggg agagccgtcg ggatgctgta tcaggtggtc 780
gatgacatca ccgaggacaa gaagaagagc tatgatggtg gagcagagaa gggaatgatg 840
gaaatggcgg aagagctcaa ggagaaggcg aagaaggagc ttcaagtgtt tgacaacaag 900
tatggaggag gagacacact tgttcctctc tacaccttcg ttgactacgc tgctcatcga 960
cattttcttc ttccctctg a 981

<210> 19

<211> 245
<212> DNA
<213> Glycine sp.

<400> 19

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tcttgcactt gcttgggtac catgatggtt gctgcatctg ctaactcttt gaatcaggtg 120
tttgagatca ataatgatgc taaaatgaag agaacaagtc gcaggccact accctcagga 180
cgcatcacaa tacctcatgc agttggctgg gcatcctctg ttggattagc tggtacggct 240
ctact 245

<210> 20
<211> 253
<212> DNA
<213> Glycine sp.

<400> 20

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ttggcattgt ccaaggatat acctgacgtt gaaggagata aagagcacgg cattgattct 120
tttgcagtac gtctaggtca gaaacgggca ttttggattt gcgtttcctt ttttgaaatg 180
gctttcggag ttggtatcct ggccggagca tcatgctcac acttttggac taaaattttc 240
acgggtatgg gaa 253

<210> 21
<211> 275
<212> DNA
<213> Glycine sp.

<400> 21

tgatcttcta ctctctgggt atggcattgt ccaaggatat atctgacgtt aaaggagata 60
aagcatacgg catcgatact ttagcgatac gtttgggtca aaaatgggta ttttggattt 120
gcattatcct ttttgaaatg gcttttggag ttgccctctt ggcaggagca acatcttctt 180
acctttggat taaaattgtc acgggtctgg gacatgctat tcttgcttca attctcttgt 240
accaagccaa atctatatac ttgagcaaca aagtt 275

<210> 22
<211> 299
<212> DNA
<213> Glycine sp.

<220>
<221> misc_feature
<222> (1)...(299)
<223> n = A,T,C or G

<400> 22

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agaagaggcc aattgtcttt ccaagatcac ttatngtggc tattgtaatc atgaacttct 120
tctttgtggg tatggcattg gcaaaggata tacctanctg ttgaaggaga taaaatatat 180
ggcattgata cttttgcaat acgtataggt caaaaacaag tattttggat ttgtattttc 240
ctttttgaaa ggctttcgga gtttccctag tggcaggagc aacatcttct agccttggt 299

<210> 23
<211> 767

<212> DNA
<213> Glycine sp.

<400> 23

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tctgatgttg aaatagacaa gataaacaag ccgtatcttc cattagcatc tggggaatat 120
tcctttgaaa ctggtgtcac tattgttgca tctttttcaa ttctgagttt ttggcttggc 180
tgggttgtag gttcatggcc attatttttgg gccctttttg taagctttgt gctaggaact 240
gcttattcaa tcaatgtgcc tctgttgaga tggaagaggt ttgcagtgct tgcagcgatg 300
tgcattctag ctgttcgggc agtaatagtt caacttgcat ttttccttca catgcagact 360
catgtgtaca agaggccacc tgtcttttca agaccattga tttttgctac tgcattcatg 420
agcttcttct ctgtagttat agcactgttt aaggatatac ctgacattga aggagataaa 480
gtatttggca tccaatcttt ttcagtgtgt ttaggtcaga agccggtgtt ctggacttgt 540
gttacccttc ttgaaatagc ttatggagtc gccctcctgg tgggagctgc atctccttgt 600
ctttggagca aaattttcac gggtctggga cacgctgtgc tggcttcaat tctctggttt 660
catgccaaat ctgtagattt gaaaagcaaa gcttcgataa catccttcta tatgtttatt 720
tggaagctat tttatgcaga atacttactc attccttttg ttagatg 767

<210> 24
<211> 255
<212> PRT
<213> Glycine sp.

<400> 24

Val Glu Ala Val Val Ala Ala Leu Phe Met Asn Ile Tyr Ile Val Gly
1 5 10 15

Leu Asn Gln Leu Ser Asp Val Glu Ile Asp Lys Ile Asn Lys Pro Tyr
20 25 30

Leu Pro Leu Ala Ser Gly Glu Tyr Ser Phe Glu Thr Gly Val Thr Ile
35 40 45

Val Ala Ser Phe Ser Ile Leu Ser Phe Trp Leu Gly Trp Val Val Gly
50 55 60

Ser Trp Pro Leu Phe Trp Ala Leu Phe Val Ser Phe Val Leu Gly Thr
65 70 75 80

Ala Tyr Ser Ile Asn Val Pro Leu Leu Arg Trp Lys Arg Phe Ala Val
85 90 95

Leu Ala Ala Met Cys Ile Leu Ala Val Arg Ala Val Ile Val Gln Leu
100 105 110

Ala Phe Phe Leu His Met Gln Thr His Val Tyr Lys Arg Pro Pro Val
115 120 125

Phe Ser Arg Pro Leu Ile Phe Ala Thr Ala Phe Met Ser Phe Phe Ser
130 135 140

Val Val Ile Ala Leu Phe Lys Asp Ile Pro Asp Ile Glu Gly Asp Lys
145 150 155 160

Val Phe Gly Ile Gln Ser Phe Ser Val Cys Leu Gly Gln Lys Pro Val
165 170 175

Phe Trp Thr Cys Val Thr Leu Leu Glu Ile Ala Tyr Gly Val Ala Leu

180 185 190

Leu Val Gly Ala Ala Ser Pro Cys Leu Trp Ser Lys Ile Phe Thr Gly
195 200 205

Leu Gly His Ala Val Leu Ala Ser Ile Leu Trp Phe His Ala Lys Ser
210 215 220

Val Asp Leu Lys Ser Lys Ala Ser Ile Thr Ser Phe Tyr Met Phe Ile
225 230 235 240

Trp Lys Leu Phe Tyr Ala Glu Tyr Leu Leu Ile Pro Phe Val Arg
245 250 255

<210> 25
<211> 360
<212> DNA
<213> Zea sp.

<220>
<221> misc_feature
<222> (1)...(360)
<223> n = A,T,C or G

<400> 25

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tcaggcttat cttggcctga cattcaactg gggagcttta ctagggtggg ctgctattaa 120
ggaaagcata gaccctgcaa atcatccttc cattgtatac agctggtatt tgttggacgc 180
tggtgtatga tactatatat gcgcatcagg tgtttcgcta tccctacttt catattaatc 240
cttgatgaag tggccatttc atgttgtcgc ggtggtctta tacttgcata tctccatgca 300
tctcaggaca aagangatga cctgaaagta ggagtccaag tccacagctt aagatttggg 360

<210> 26
<211> 299
<212> DNA
<213> Zea sp.

<220>
<221> misc_feature
<222> (1)...(299)
<223> n = A,T,C or G

<400> 26

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aatgaaaagg acaatgcgtg ccccctgcca tctggtcgca ttagtcctgc acatgctgcg 120
atgtgggcta caagtgttgg agttgcagga acagctttgt tggcctggaa ggctaatggc 180
ttggcagctg ggcttgcagc ttctaatctt gttctgtatg catttgtgta tacgccgttg 240
aagcaaatac accctgttaa tacatgggtt ggggcagtcg ttggtgccat cccaccact 299

<210> 27
<211> 255
<212> DNA
<213> Zea sp.

<220>
<221> misc_feature
<222> (1)...(255)

<223> n = A,T,C or G

<400> 27

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tgcttcggca gcttagcact cagtggttac aatgctgacc ttggttggtg tttagtgtga 180
tgcttgagcg aagaatggta tngtttttac ttgatattga ctccagacct gaaatcatgt 240
tggacagggt ggccc 255

<210> 28
<211> 257
<212> DNA
<213> Zea sp.

<400> 28

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gcaaaatgga tttgtgttgg agcaattgat atcactcaat tatctgttgc aggttaccta 120
ttgagcaccg gtaagctgta ttatgccctg gtgttgcttg ggctaacaat tcctcaggtg 180
ttctttcagt tccagtactt cctgaaggac cctgtgaagt atgatgtcaa atatcaggca 240
agcgcacaac cattctt 257

<210> 29
<211> 368
<212> DNA
<213> Zea sp.

<400> 29

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cctgacatcg aaggggaccg catattcggg atccgatcct tcagcgtccg gttagggcaa 120
aagaaggtct tttggatctg cgttggcttg cttgagatgg cctacagcgt tgcgatactg 180
atgggagcta cctcttcctg tttgtggagc aaaacagcaa ccatcgctgg ccattccata 240
cttgccgcga tcctatggag ctgcgcgcga tcggtggact tgacgagcaa agccgcaata 300
acgtccttct acatgttcat ctggaagctg ttctacgcgg agtacctgct catccctctg 360
gtgcggtg 368

<210> 30
<211> 122
<212> PRT
<213> Zea sp.

<400> 30

Ile Gln Leu Gln Ile Ile Met Ala Phe Phe Ser Val Val Ile Ala Leu
1 5 10 15

Phe Lys Asp Ile Pro Asp Ile Glu Gly Asp Arg Ile Phe Gly Ile Arg
20 25 30

Ser Phe Ser Val Arg Leu Gly Gln Lys Lys Val Phe Trp Ile Cys Val
35 40 45

Gly Leu Leu Glu Met Ala Tyr Ser Val Ala Ile Leu Met Gly Ala Thr
50 55 60

Ser Ser Cys Leu Trp Ser Lys Thr Ala Thr Ile Ala Gly His Ser Ile

65 70 75 80

Leu Ala Ala Ile Leu Trp Ser Cys Ala Arg Ser Val Asp Leu Thr Ser
85 90 95

Lys Ala Ala Ile Thr Ser Phe Tyr Met Phe Ile Trp Lys Leu Phe Tyr
100 105 110

Ala Glu Tyr Leu Leu Ile Pro Leu Val Arg
115 120

<210> 31
<211> 278
<212> DNA
<213> Zea sp.

<400> 31

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gcgagttaca tcagcttgcc ctggtgggct ggccaggcgt tatttggaac tcttacacca 120
gatatcattg tcttgactac tttgtacagc atagctgggc tagggattgc tattgtaaat 180
gatttcaaga gtattgaagg ggataggact ctggggcttc agtcacttcc tgttgctttt 240
gggatggaaa ctgcaaaatg gatttgtgtt ggagcaat 278

<210> 32
<211> 292
<212> PRT
<213> Synechocystis sp.

<400> 32

Met Val Ala Gln Thr Pro Ser Ser Pro Pro Leu Trp Leu Thr Ile Ile
1 5 10 15

Tyr Leu Leu Arg Trp His Lys Pro Ala Gly Arg Leu Ile Leu Met Ile
20 25 30

Pro Ala Leu Trp Ala Val Cys Leu Ala Ala Gln Gly Leu Pro Pro Leu
35 40 45

Pro Leu Leu Gly Thr Ile Ala Leu Gly Thr Leu Ala Thr Ser Gly Leu
50 55 60

Gly Cys Val Val Asn Asp Leu Trp Asp Arg Asp Ile Asp Pro Gln Val
65 70 75 80

Glu Arg Thr Lys Gln Arg Pro Leu Ala Ala Arg Ala Leu Ser Val Gln
85 90 95

Val Gly Ile Gly Val Ala Leu Val Ala Leu Leu Cys Ala Ala Gly Leu
100 105 110

Ala Phe Tyr Leu Thr Pro Leu Ser Phe Trp Leu Cys Val Ala Ala Val
115 120 125

Pro Val Ile Val Ala Tyr Pro Gly Ala Lys Arg Val Phe Pro Val Pro
130 135 140

Gln Leu Val Leu Ser Ile Ala Trp Gly Phe Ala Val Leu Ile Ser Trp

145 150 155 160

Ser Ala Val Thr Gly Asp Leu Thr Asp Ala Thr Trp Val Leu Trp Gly
165 170 175

Ala Thr Val Phe Trp Thr Leu Gly Phe Asp Thr Val Tyr Ala Met Ala
180 185 190

Asp Arg Glu Asp Asp Arg Arg Ile Gly Val Asn Ser Ser Ala Leu Phe
195 200 205

Phe Gly Gln Tyr Val Gly Glu Ala Val Gly Ile Phe Phe Ala Leu Thr
210 215 220

Ile Gly Cys Leu Phe Tyr Leu Gly Met Ile Leu Met Leu Asn Pro Leu
225 230 235 240

Tyr Trp Leu Ser Leu Ala Ile Ala Ile Val Gly Trp Val Ile Gln Tyr
245 250 255

Ile Gln Leu Ser Ala Pro Thr Pro Glu Pro Lys Leu Tyr Gly Gln Ile
260 265 270

Phe Gly Gln Asn Val Ile Ile Gly Phe Val Leu Leu Ala Gly Met Leu
275 280 285

Leu Gly Trp Leu
290

<210> 33
<211> 316
<212> PRT
<213> Synechocystis sp.

<400> 33

Met Val Thr Ser Thr Lys Ile His Arg Gln His Asp Ser Met Gly Ala
1 5 10 15

Val Cys Lys Ser Tyr Tyr Gln Leu Thr Lys Pro Arg Ile Ile Pro Leu
20 25 30

Leu Leu Ile Thr Thr Ala Ala Ser Met Trp Ile Ala Ser Glu Gly Arg
35 40 45

Val Asp Leu Pro Lys Leu Leu Ile Thr Leu Leu Gly Gly Thr Leu Ala
50 55 60

Ala Ala Ser Ala Gln Thr Leu Asn Cys Ile Tyr Asp Gln Asp Ile Asp
65 70 75 80

Tyr Glu Met Leu Arg Thr Arg Ala Arg Pro Ile Pro Ala Gly Lys Val
85 90 95

Gln Pro Arg His Ala Leu Ile Phe Ala Leu Ala Leu Gly Val Leu Ser
100 105 110

Phe Ala Leu Leu Ala Thr Phe Val Asn Val Leu Ser Gly Cys Leu Ala
115 120 125

Leu Ser Gly Ile Val Phe Tyr Met Leu Val Tyr Thr His Trp Leu Lys
130 135 140

Arg His Thr Ala Gln Asn Ile Val Ile Gly Gly Ala Ala Gly Ser Ile
145 150 155 160

Pro Pro Leu Val Gly Trp Ala Ala Val Thr Gly Asp Leu Ser Trp Thr
165 170 175

Pro Trp Val Leu Phe Ala Leu Ile Phe Leu Trp Thr Pro Pro His Phe
180 185 190

Trp Ala Leu Ala Leu Met Ile Lys Asp Asp Tyr Ala Gln Val Asn Val
195 200 205

Pro Met Leu Pro Val Ile Ala Gly Glu Glu Lys Thr Val Ser Gln Ile
210 215 220

Trp Tyr Tyr Ser Leu Leu Val Val Pro Phe Ser Leu Leu Leu Val Tyr
225 230 235 240

Pro Leu His Gln Leu Gly Ile Leu Tyr Leu Ala Ile Ala Ile Ile Leu
245 250 255

Gly Gly Gln Phe Leu Val Lys Ala Trp Gln Leu Lys Gln Ala Pro Gly
260 265 270

Asp Arg Asp Leu Ala Arg Gly Leu Phe Lys Phe Ser Ile Phe Tyr Leu
275 280 285

Met Leu Leu Cys Leu Ala Met Val Ile Asp Ser Leu Pro Val Thr His
290 295 300

Gln Leu Val Ala Gln Met Gly Thr Leu Leu Leu Gly
305 310 315

<210> 34
<211> 324
<212> PRT
<213> Synechocystis sp.

<400> 34

Met Ser Asp Thr Gln Asn Thr Gly Gln Asn Gln Ala Lys Ala Arg Gln
1 5 10 15

Leu Leu Gly Met Lys Gly Ala Ala Pro Gly Glu Ser Ser Ile Trp Lys
20 25 30

Ile Arg Leu Gln Leu Met Lys Pro Ile Thr Trp Ile Pro Leu Ile Trp
35 40 45

Gly Val Val Cys Gly Ala Ala Ser Ser Gly Gly Tyr Ile Trp Ser Val
50 55 60

Glu Asp Phe Leu Lys Ala Leu Thr Cys Met Leu Leu Ser Gly Pro Leu
65 70 75 80

Met Thr Gly Tyr Thr Gln Thr Leu Asn Asp Phe Tyr Asp Arg Asp Ile
85 90 95

Asp Ala Ile Asn Glu Pro Tyr Arg Pro Ile Pro Ser Gly Ala Ile Ser
100 105 110

Val Pro Gln Val Val Thr Gln Ile Leu Ile Leu Leu Val Ala Gly Ile
115 120 125

Gly Val Ala Tyr Gly Leu Asp Val Trp Ala Gln His Asp Phe Pro Ile
130 135 140

Met Met Val Leu Thr Leu Gly Gly Ala Phe Val Ala Tyr Ile Tyr Ser
145 150 155 160

Ala Pro Pro Leu Lys Leu Lys Gln Asn Gly Trp Leu Gly Asn Tyr Ala
165 170 175

Leu Gly Ala Ser Tyr Ile Ala Leu Pro Trp Trp Ala Gly His Ala Leu
180 185 190

Phe Gly Thr Leu Asn Pro Thr Ile Met Val Leu Thr Leu Ile Tyr Ser
195 200 205

Leu Ala Gly Leu Gly Ile Ala Val Val Asn Asp Phe Lys Ser Val Glu
210 215 220

Gly Asp Arg Gln Leu Gly Leu Lys Ser Leu Pro Val Met Phe Gly Ile
225 230 235 240

Gly Thr Ala Ala Trp Ile Cys Val Ile Met Ile Asp Val Phe Gln Ala
245 250 255

Gly Ile Ala Gly Tyr Leu Ile Tyr Val His Gln Gln Leu Tyr Ala Thr
260 265 270

Ile Val Leu Leu Leu Leu Ile Pro Gln Ile Thr Phe Gln Asp Met Tyr
275 280 285

Phe Leu Arg Asn Pro Leu Glu Asn Asp Val Lys Tyr Gln Ala Ser Ala
290 295 300

Gln Pro Phe Leu Val Phe Gly Met Leu Ala Thr Gly Leu Ala Leu Gly
305 310 315 320

His Ala Gly Ile

<210> 35
<211> 307
<212> PRT
<213> Synechocystis sp.

<400> 35

Met Thr Glu Ser Ser Pro Leu Ala Pro Ser Thr Ala Pro Ala Thr Arg
1 5 10 15

Lys Leu Trp Leu Ala Ala Ile Lys Pro Pro Met Tyr Thr Val Ala Val
20 25 30

Val Pro Ile Thr Val Gly Ser Ala Val Ala Tyr Gly Leu Thr Gly Gln
35 40 45

Trp His Gly Asp Val Phe Thr Ile Phe Leu Leu Ser Ala Ile Ala Ile
50 55 60

Ile Ala Trp Ile Asn Leu Ser Asn Asp Val Phe Asp Ser Asp Thr Gly
65 70 75 80

Ile Asp Val Arg Lys Ala His Ser Val Val Asn Leu Thr Gly Asn Arg
85 90 95

Asn Leu Val Phe Leu Ile Ser Asn Phe Phe Leu Leu Ala Gly Val Leu
100 105 110

Gly Leu Met Ser Met Ser Trp Arg Ala Gln Asp Trp Thr Val Leu Glu
115 120 125

Leu Ile Gly Val Ala Ile Phe Leu Gly Tyr Thr Tyr Gln Gly Pro Pro
130 135 140

Phe Arg Leu Gly Tyr Leu Gly Leu Gly Glu Leu Ile Cys Leu Ile Thr
145 150 155 160

Phe Gly Pro Leu Ala Ile Ala Ala Ala Tyr Tyr Ser Gln Ser Gln Ser
165 170 175

Phe Ser Trp Asn Leu Leu Thr Pro Ser Val Phe Val Gly Ile Ser Thr
180 185 190

Ala Ile Ile Leu Phe Cys Ser His Phe His Gln Val Glu Asp Asp Leu
195 200 205

Ala Ala Gly Lys Lys Ser Pro Ile Val Arg Leu Gly Thr Lys Leu Gly
210 215 220

Ser Gln Val Leu Thr Leu Ser Val Val Ser Leu Tyr Leu Ile Thr Ala
225 230 235 240

Ile Gly Val Leu Cys His Gln Ala Pro Trp Gln Thr Leu Leu Ile Ile
245 250 255

Ala Ser Leu Pro Trp Ala Val Gln Leu Ile Arg His Val Gly Gln Tyr
260 265 270

His Asp Gln Pro Glu Gln Val Ser Asn Cys Lys Phe Ile Ala Val Asn
275 280 285

Leu His Phe Phe Ser Gly Met Leu Met Ala Ala Gly Tyr Gly Trp Ala
290 295 300

Gly Leu Gly
305

<210> 36
<211> 927
<212> DNA
<213> Synechocystis sp.

<400> 36

atggcaacta tccaagcttt ttggcgcttc tcccgccccc ataccatcat tggtacaact 60

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cctgcttccc tggatttagt gttcggcgct tggctggcct gcctgttggg taatgtgtac 180
attgtcggcc tcaaccaatt gtgggatgtg gacattgacc gcatcaataa gccgaatttg 240
cccctagcta acggagattt ttctatcgcc cagggccgtt ggattgtggg actttgtggc 300
gttgcttcct tggcgatcgc ctggggatta gggctatggc tggggctaac ggtgggcatt 360
agtttgatta ttggcacggc ctattcggtg ccgccagtga ggttaaagcg cttttccctg 420
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ttttttagaa ttggtttagg ttatcccccc actttaataa cccccatctg ggttttgact 540
ttatttatct tagttttcac cgtggcgatc gccattttta aagatgtgcc agatatggaa 600
ggcgatcggc aatttaagat tcaaacttta actttgcaaa tcggcaaaca aaacgttttt 660
cggggaacct taattttact cactggttgt tatttagcca tggcaatctg gggcttatgg 720
gcggctatgc ctttaaatac tgctttcttg attgtttccc atttgtgctt attagcctta 780
ctctggtggc ggagtcgaga tgtacactta gaaagcaaaa ccgaaattgc tagttttat 840
cagtttattt ggaagctatt tttcttagag tacttgctgt atcccttggc tctgtggtta 900
cctaattttt ctaatactat tttttag 927

<210> 37
<211> 308
<212> PRT
<213> Synechocystis sp.

<400> 37

Met Ala Thr Ile Gln Ala Phe Trp Arg Phe Ser Arg Pro His Thr Ile
1 5 10 15

Ile Gly Thr Thr Leu Ser Val Trp Ala Val Tyr Leu Leu Thr Ile Leu
20 25 30

Gly Asp Gly Asn Ser Val Asn Ser Pro Ala Ser Leu Asp Leu Val Phe
35 40 45

Gly Ala Trp Leu Ala Cys Leu Leu Gly Asn Val Tyr Ile Val Gly Leu
50 55 60

Asn Gln Leu Trp Asp Val Asp Ile Asp Arg Ile Asn Lys Pro Asn Leu
65 70 75 80

Pro Leu Ala Asn Gly Asp Phe Ser Ile Ala Gln Gly Arg Trp Ile Val
85 90 95

Gly Leu Cys Gly Val Ala Ser Leu Ala Ile Ala Trp Gly Leu Gly Leu
100 105 110

Trp Leu Gly Leu Thr Val Gly Ile Ser Leu Ile Ile Gly Thr Ala Tyr
115 120 125

Ser Val Pro Pro Val Arg Leu Lys Arg Phe Ser Leu Leu Ala Ala Leu
130 135 140

Cys Ile Leu Thr Val Arg Gly Ile Val Val Asn Leu Gly Leu Phe Leu
145 150 155 160

Phe Phe Arg Ile Gly Leu Gly Tyr Pro Pro Thr Leu Ile Thr Pro Ile
165 170 175

Trp Val Leu Thr Leu Phe Ile Leu Val Phe Thr Val Ala Ile Ala Ile
180 185 190

Phe Lys Asp Val Pro Asp Met Glu Gly Asp Arg Gln Phe Lys Ile Gln

195 200 205

Thr Leu Thr Leu Gln Ile Gly Lys Gln Asn Val Phe Arg Gly Thr Leu
210 215 220

Ile Leu Leu Thr Gly Cys Tyr Leu Ala Met Ala Ile Trp Gly Leu Trp
225 230 235 240

Ala Ala Met Pro Leu Asn Thr Ala Phe Leu Ile Val Ser His Leu Cys
245 250 255

Leu Leu Ala Leu Leu Trp Trp Arg Ser Arg Asp Val His Leu Glu Ser
260 265 270

Lys Thr Glu Ile Ala Ser Phe Tyr Gln Phe Ile Trp Lys Leu Phe Phe
275 280 285

Leu Glu Tyr Leu Leu Tyr Pro Leu Ala Leu Trp Leu Pro Asn Phe Ser
290 295 300

Asn Thr Ile Phe
305

<210> 38
<211> 1092
<212> DNA
<213> Synechocystis sp.

<400> 38

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tggtacgtgc gcctgctttt gccccaatcc ggggaaagtt ttgcttttat gtactccatc 120
gaaaatcctg ctagcgatca tcattacggc ggcggtgctg tgcaaatttt agggccggct 180
acgaaaaaac aagaaaatca ggaagaccaa cttgtttggc ggacatttcc ctcggtaaaa 240
aaattttggg ccagtcctcg ccagtttgcc ctagggcatt ggggaaaatg tagggataac 300
aggcaggcga aacccctact ctccgaagaa ttttttgcca cggtcaagga aggttatcaa 360
atccatcaaa atcagcacca aggacaaatc attcatggcg atcgccattg tcgttggcag 420
ttcaccgtag aaccggaagt aacttggggg agtcctaacc gatttcctcg ggctacagcg 480
ggttggcttt ccttttacc cttgtttgat cccggttggc aaattctttt agcccaaggt 540
agagcgcacg gctggctgaa atggcagagg gaacagtatg aatttgacca cgccctagtt 600
tatgccgaaa aaaattgggg tcactccttt ccctcccgct ggttttggct ccaagcaaat 660
tattttcctg accatccagg actgagcgtc actgccgctg gcggggaacg gattgttctt 720
ggtcgccccg aagaggtagc tttaattggc ttacatcacc aaggtaattt ttacgaattt 780
ggcccgggcc atggcacagt cacttggcaa gtagctccct ggggccgttg gcaattaaaa 840
gccagcaatg ataggtattg ggtcaagttg tccggaaaaa cagataaaaa aggcagttta 900
gtccacactc ccaccgccca gggcttacaa ctcaactgcc gagataccac taggggctat 960
ttgtatttgc aattgggatc tgtgggtcac ggcctgatag tgcaagggga aacggacacc 1020
gcggggctag aagttggagg tgattggggt ttaacagagg aaaatttgag caaaaaaaca 1080
gtgccattct ga 1092

<210> 39
<211> 363
<212> PRT
<213> Synechocystis sp.

<400> 39

Met Lys Phe Pro Pro His Ser Gly Tyr His Trp Gln Gly Gln Ser Pro
1 5 10 15

Phe Phe Glu Gly Trp Tyr Val Arg Leu Leu Leu Pro Gln Ser Gly Glu
20 25 30

Ser Phe Ala Phe Met Tyr Ser Ile Glu Asn Pro Ala Ser Asp His His
35 40 45

Tyr Gly Gly Gly Ala Val Gln Ile Leu Gly Pro Ala Thr Lys Lys Gln
50 55 60

Glu Asn Gln Glu Asp Gln Leu Val Trp Arg Thr Phe Pro Ser Val Lys
65 70 75 80

Lys Phe Trp Ala Ser Pro Arg Gln Phe Ala Leu Gly His Trp Gly Lys
85 90 95

Cys Arg Asp Asn Arg Gln Ala Lys Pro Leu Leu Ser Glu Glu Phe Phe
100 105 110

Ala Thr Val Lys Glu Gly Tyr Gln Ile His Gln Asn Gln His Gln Gly
115 120 125

Gln Ile Ile His Gly Asp Arg His Cys Arg Trp Gln Phe Thr Val Glu
130 135 140

Pro Glu Val Thr Trp Gly Ser Pro Asn Arg Phe Pro Arg Ala Thr Ala
145 150 155 160

Gly Trp Leu Ser Phe Leu Pro Leu Phe Asp Pro Gly Trp Gln Ile Leu
165 170 175

Leu Ala Gln Gly Arg Ala His Gly Trp Leu Lys Trp Gln Arg Glu Gln
180 185 190

Tyr Glu Phe Asp His Ala Leu Val Tyr Ala Glu Lys Asn Trp Gly His
195 200 205

Ser Phe Pro Ser Arg Trp Phe Trp Leu Gln Ala Asn Tyr Phe Pro Asp
210 215 220

His Pro Gly Leu Ser Val Thr Ala Ala Gly Gly Glu Arg Ile Val Leu
225 230 235 240

Gly Arg Pro Glu Glu Val Ala Leu Ile Gly Leu His His Gln Gly Asn
245 250 255

Phe Tyr Glu Phe Gly Pro Gly His Gly Thr Val Thr Trp Gln Val Ala
260 265 270

Pro Trp Gly Arg Trp Gln Leu Lys Ala Ser Asn Asp Arg Tyr Trp Val
275 280 285

Lys Leu Ser Gly Lys Thr Asp Lys Lys Gly Ser Leu Val His Thr Pro
290 295 300

Thr Ala Gln Gly Leu Gln Leu Asn Cys Arg Asp Thr Thr Arg Gly Tyr
305 310 315 320

Leu Tyr Leu Gln Leu Gly Ser Val Gly His Gly Leu Ile Val Gln Gly
325 330 335

Glu Thr Asp Thr Ala Gly Leu Glu Val Gly Gly Asp Trp Gly Leu Thr
340 345 350

Glu Glu Asn Leu Ser Lys Lys Thr Val Pro Phe
355 360

<210> 40
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide adapter

<400> 40

cgcgatttaa atggcgcgcc ctgcaggcgg ccgcctgcag ggcgcgccat ttaaat 56

<210> 41
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 41

tcgaggatcc gcggccgcaa gcttcctgca gg 32

<210> 42
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 42

tcgacctgca ggaagcttgc ggccgcggat cc 32

<210> 43
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 43

tcgacctgca ggaagcttgc ggccgcggat cc 32

<210> 44
<211> 32

<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 44

tcgaggatcc gcggccgcaa gcttcctgca gg 32

<210> 45
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 45

tcgaggatcc gcggccgcaa gcttcctgca ggagct 36

<210> 46
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 46

cctgcaggaa gcttgcggcc gcggatcc 28

<210> 47
<211> 36
<212> DNA
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<220>
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<400> 47

tcgacctgca ggaagcttgc ggccgcggat ccagct 36

<210> 48
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 48

ggatccgcgg ccgcaagctt cctgcagg 28

<210> 49
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 49
gatcacctgc aggaagcttg cggccgcgga tccaatgca 39

<210> 50
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 50
ttggatccgc ggccgcaagc ttcctgcagg t 31

<210> 51
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotides

<400> 51
ggatccgcgg ccgcacaatg gagtctctgc tctctagttc t 41

<210> 52
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotides

<400> 52
ggatcctgca ggtcacttca aaaaaggtaa cagcaagt 38

<210> 53
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotides

<400> 53

ggatccgcgg ccgcacaatg gcgtttttttg ggctctcccg tgttt 45

<210> 54
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotides

<400> 54

ggatcctgca ggttattgaa aacttcttcc aagtacaact 40

<210> 55
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotides

<400> 55

ggatccgcgg ccgcacaatg tggcgaagat ctgttgtt 38

<210> 56
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotides

<400> 56

ggatcctgca ggtcatggag agtagaagga aggagct 37

<210> 57
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotides

<400> 57

ggatccgcgg ccgcacaatg gtacttgccg aggttccaaa gcttgcctct 50

<210> 58
<211> 38
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotides

<400> 58

ggatcctgca ggtcacttgt ttctggtgat gactctat 38

<210> 59
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotides

<400> 59

ggatccgcgg ccgcacaatg acttcgattc tcaacact 38

<210> 60
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotides

<400> 60

ggatcctgca ggtcagtgtt gcgatgctaa tgccgt 36

<210> 61
<211> 22
<212> DNA
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<220>
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<400> 61

taatgtgtac attgtcggcc tc 22

<210> 62
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Region of slr1736 open reading frame

<400> 62

gcaatgtaac atcagagatt ttgagacaca acgtggcttt ccacaattcc ccgcaccgtc 60

<210> 63
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Region of slr1736 open reading frame

<400> 63
aggctaataa gcacaaatgg ga 22

<210> 64
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<212> DNA
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<220>
<223> Region of slr1736 open reading frame

<400> 64
ggtatgagtc agcaacacct tcttcacgag gcagacctca gcggaattgg tttaggttat 60
ccc 63

<210> 65
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 65
ggatccatgg ttgcccaaac cccatc 26

<210> 66
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 66
gcaatgtaac atcagagatt ttgagacaca acgtggcttt gggtaagcaa caatgaccgg 60
c 61

<210> 67
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide primer

<400> 67

gaattctcaa agccagccca gtaac 25

<210> 68
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 68

ggtatgagtc agcaacacct tcttcacgag gcagacctca gcgggtgcga aaagggtttt 60
ccc 63

<210> 69
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<400> 69

ccagtggttt aggctgtgtg gtc 23

<210> 70
<211> 21
<212> DNA
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<220>
<223> End of open reading frame fragment

<400> 70

ctgagttgga tgtattggat c 21

<210> 71
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 71

ggatccatgg ttacttcgac aaaaatcc 28

<210> 72

<211> 60
<212> DNA
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<220>
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<400> 72

gcaatgtaac atcagagatt ttgagacaca acgtggcttt gctaggcaac cgcttagtac 60

<210> 73
<211> 28
<212> DNA
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<220>
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<400> 73

gaattcttaa cccaacagta aagttccc 28

<210> 74
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 74

ggtatgagtc agcaacacct tcttcacgag gcagacctca gcgccggcat tgtcttttac 60
atg 63

<210> 75
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Open reading frame fragment

<400> 75

ggaacccttg cagccgcttc 20

<210> 76
<211> 22
<212> DNA
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<400> 76

gtatgcccaa ctggtgcaga gg 22

<210> 77
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
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<400> 77
ggatccatgt ctgacacaca aaataccg 28

<210> 78
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
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<400> 78
gcaatgtaac atcagagatt ttgagacaca acgtggcttt cgccaatacc agccaccaac 60
ag 62

<210> 79
<211> 27
<212> DNA
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<220>
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<400> 79
gaattctcaa atccccgcat ggcctag 27

<210> 80
<211> 65
<212> DNA
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<220>
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<400> 80
ggtatgagtc agcaacacct tcttcacgag gcagacctca gcggcctacg gcttggacgt 60
gtggg 65

<210> 81
<211> 21
<212> DNA
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<220>
<223> Open reading frame fragment

<400> 81
cacttggatt cccctgatct g 21

<210> 82
<211> 21
<212> DNA
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<220>
<223> Open reading frame fragment

<400> 82
gcaatacccg cttggaaaac g 21

<210> 83
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
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<400> 83
ggatccatga ccgaatcttc gcccctagc 29

<210> 84
<211> 61
<212> DNA
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<220>
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<400> 84
gcaatgtaac atcagagatt ttgagacaca acgtggcttt caatcctagg tagccgaggc g 60 61

<210> 85
<211> 27
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<220>
<223> Synthetic oligonucleotide primer

<400> 85
gaattcttag cccaggccag cccagcc 27

<210> 86
<211> 66
<212> DNA
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<220>
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<400> 86

ggtatgagtc agcaacacct tcttcacgag gcagacctca gcggggaatt gatttgttta 60
attacc 66

<210> 87
<211> 21
<212> DNA
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<400> 87

gcgatcgcca ttatcgcttg g 21

<210> 88
<211> 24
<212> DNA
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<220>
<223> Open reading frame fragment

<400> 88

gcagactggc aattatcagt aacg 24

<210> 89
<211> 25
<212> DNA
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<220>
<223> Primer

<400> 89

ccatggattc gagtaaagtt gtcgc 25

<210> 90
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 90

gaattcactt caaaaaaggt aacag

<210> 91
<211> 4550
<212> DNA
<213> Arabidopsis sp.

<400> 91

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cgattaagat taggaaaaat ttataaccgg taattaagaa aacattaacc gtagtaaccg 180
taaatgccga ttcctcccct gtctaaaaga cagaaaacat atattttatt ttgccccata 240
tgtttcactc tatttaattt caggcacaat acttttggtt ggtaacaaaa ctaaaaagga 300
caacacgtga tacttttcct cgtccgtcag tcagattttt tttaaactag aaacaagtgg 360
caaatctaca ccacattttt tgcttaatct attaacttgt aagttttaaa ttcctaaaaa 420
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taattttcaa aatctaatct aaatatctaa taattcaaaa tcattaaaaa gacacgcaac 540
aatgacacca attaatcatc ctcgacccac acaattctac agttctcatg ctaaaccata 600
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aatactcaat catcttagtc tcattattct attggttgaa tcacattttc taatttggaa 1140
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gttactgatg ttgtttagct ctttacacca atatatacac ccaattttgc agaaatccga 1260
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aagtttctct ttaaaaatgt aactctttta aaacgcaatc tttcagggtt ttcaaggaga 1560
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<211> 1236
<212> DNA
<213> Glycine sp.

<400> 95

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<210> 96
<211> 1188
<212> DNA
<213> Glycine sp.

<400> 96

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<211> 395
<212> PRT
<213> Glycine sp.

<400> 97

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35 40 45

Leu Asn His His Tyr Lys Ser Ile Glu Gly Gly Cys Thr Cys Lys Lys
50 55 60

Cys Asn Ile Lys Phe Val Val Lys Ala Thr Ser Glu Lys Ser Phe Glu
65 70 75 80

Ser Glu Pro Gln Ala Phe Asp Pro Lys Ser Ile Leu Asp Ser Val Lys
85 90 95

Asn Ser Leu Asp Ala Phe Tyr Arg Phe Ser Arg Pro His Thr Val Ile
100 105 110

Gly Thr Ala Leu Ser Ile Ile Ser Val Ser Leu Leu Ala Val Glu Lys
115 120 125

Ile Ser Asp Ile Ser Pro Leu Phe Phe Thr Gly Val Leu Glu Ala Val
130 135 140

Val Ala Ala Leu Phe Met Asn Ile Tyr Ile Val Gly Leu Asn Gln Leu
145 150 155 160

Ser Asp Val Glu Ile Asp Lys Ile Asn Lys Pro Tyr Leu Pro Leu Ala
165 170 175

Ser Gly Glu Tyr Ser Phe Glu Thr Gly Val Thr Ile Val Ala Ser Phe
180 185 190

Ser Ile Leu Ser Phe Trp Leu Gly Trp Val Val Gly Ser Trp Pro Leu
195 200 205

Phe Trp Ala Leu Phe Val Ser Phe Val Leu Gly Thr Ala Tyr Ser Ile
210 215 220

Asn Val Pro Leu Leu Arg Trp Lys Arg Phe Ala Val Leu Ala Ala Met
225 230 235 240

Cys Ile Leu Ala Val Arg Ala Val Ile Val Gln Leu Ala Phe Phe Leu
245 250 255

His Ile Gln Thr His Val Tyr Lys Arg Pro Pro Val Phe Ser Arg Ser
260 265 270

Leu Ile Phe Ala Thr Ala Phe Met Ser Phe Phe Ser Val Val Ile Ala
275 280 285

Leu Phe Lys Asp Ile Pro Asp Ile Glu Gly Asp Lys Val Phe Gly Ile
290 295 300

Gln Ser Phe Ser Val Arg Leu Gly Gln Lys Pro Val Phe Trp Thr Cys
305 310 315 320

Val Ile Leu Leu Glu Ile Ala Tyr Gly Val Ala Leu Leu Val Gly Ala

325 330 335

Ala Ser Pro Cys Leu Trp Ser Lys Ile Val Thr Gly Leu Gly His Ala
340 345 350

Val Leu Ala Ser Ile Leu Trp Phe His Ala Lys Ser Val Asp Leu Lys
355 360 365

Ser Lys Ala Ser Ile Thr Ser Phe Tyr Met Phe Ile Trp Lys Leu Phe
370 375 380

Tyr Ala Glu Tyr Leu Leu Ile Pro Phe Val Arg
385 390 395

<210> 98
<211> 411
<212> PRT
<213> Glycine sp.

<400> 98

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Ser Leu Thr Thr Thr Gly Ala Asn Phe Ser Arg Thr Lys Ser Phe Ala
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Asn Ile Tyr His Ala Ser Ser Tyr Val Pro Asn Ala Ser Trp His Asn
35 40 45

Arg Lys Ile Gln Lys Glu Tyr Asn Phe Leu Arg Phe Arg Trp Pro Ser
50 55 60

Leu Asn His His Tyr Lys Gly Ile Glu Gly Ala Cys Thr Cys Lys Lys
65 70 75 80

Cys Asn Ile Lys Phe Val Val Lys Ala Thr Ser Glu Lys Ser Leu Glu
85 90 95

Ser Glu Pro Gln Ala Phe Asp Pro Lys Ser Ile Leu Asp Ser Val Lys
100 105 110

Asn Ser Leu Asp Ala Phe Tyr Arg Phe Ser Arg Pro His Thr Val Ile
115 120 125

Gly Thr Ala Leu Ser Ile Ile Ser Val Ser Leu Leu Ala Val Glu Lys
130 135 140

Ile Ser Asp Ile Ser Pro Leu Phe Phe Thr Gly Val Leu Glu Ala Val
145 150 155 160

Val Ala Ala Leu Phe Met Asn Ile Tyr Ile Val Gly Leu Asn Gln Leu
165 170 175

Ser Asp Val Glu Ile Asp Lys Ile Asn Lys Pro Tyr Leu Pro Leu Ala
180 185 190

Ser Gly Glu Tyr Ser Phe Glu Thr Gly Val Thr Ile Val Ala Ser Phe
195 200 205

Ser Ile Leu Ser Phe Trp Leu Gly Trp Val Val Gly Ser Trp Pro Leu
210 215 220

Phe Trp Ala Leu Phe Val Ser Phe Val Leu Gly Thr Ala Tyr Ser Ile
225 230 235 240

Asn Val Pro Leu Leu Arg Trp Lys Arg Phe Ala Val Leu Ala Ala Met
245 250 255

Cys Ile Leu Ala Val Arg Ala Val Ile Val Gln Leu Ala Phe Phe Leu
260 265 270

His Met Gln Thr His Val Tyr Lys Arg Pro Pro Val Phe Ser Arg Pro
275 280 285

Leu Ile Phe Ala Thr Ala Phe Met Ser Phe Phe Ser Val Val Ile Ala
290 295 300

Leu Phe Lys Asp Ile Pro Asp Ile Glu Gly Asp Lys Val Phe Gly Ile
305 310 315 320

Gln Ser Phe Ser Val Arg Leu Gly Gln Lys Pro Val Phe Trp Thr Cys
325 330 335

Val Thr Leu Leu Glu Ile Ala Tyr Gly Val Ala Leu Leu Val Gly Ala
340 345 350

Ala Ser Pro Cys Leu Trp Ser Lys Ile Phe Thr Gly Leu Gly His Ala
355 360 365

Val Leu Ala Ser Ile Leu Trp Phe His Ala Lys Ser Val Asp Leu Lys
370 375 380

Ser Lys Ala Ser Ile Thr Ser Phe Tyr Met Phe Ile Trp Lys Leu Phe
385 390 395 400

Tyr Ala Glu Tyr Leu Leu Ile Pro Phe Val Arg
405 410

<210> 99
<211> 964
<212> DNA
<213> Oryza sp.

<400> 99

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gtgt 964

<210> 100
<211> 421
<212> DNA
<213> Triticum sp.

<400> 100

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c 421

<210> 101
<211> 705
<212> DNA
<213> Allium porrum

<400> 101

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<210> 102
<211> 637
<212> DNA
<213> Allium porrum

<220>
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<400> 102

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<210> 103
<211> 677
<212> DNA
<213> Brassica napus

<400> 103

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cggacgcgtg ggtcgac 677

<210> 104
<211> 1431
<212> DNA
<213> Zea sp.

<400> 104

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<210> 105
<211> 1870
<212> DNA
<213> Zea sp.

<400> 105

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<210> 106
<211> 642
<212> DNA
<213> Zea sp.

<400> 106

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<210> 107
<211> 362
<212> DNA
<213> Gossypium sp.

<400> 107

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gt 362

<210> 108
<211> 575
<212> DNA
<213> Lycopersicon sp.

<400> 108

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<211> 1663
<212> DNA
<213> Arabidopsis sp.

<400> 109

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<210> 110
<211> 488
<212> PRT
<213> Arabidopsis sp.

<400> 110

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Phe Glu Leu Ser Arg Pro Val Ser Pro Leu Thr Arg Ser Leu Val Pro
            20                  25                  30

Phe Arg Ser Thr Lys Leu Val Pro Arg Ser Ile Ser Arg Val Ser Ala
        35                  40                  45

Ser Ile Ser Thr Pro Asn Ser Glu Thr Asp Lys Ile Ser Val Lys Pro
    50                  55                  60

Val Tyr Val Pro Thr Ser Pro Asn Arg Glu Leu Arg Thr Pro His Ser
65                  70                  75                  80

Gly Tyr His Phe Asp Gly Thr Pro Arg Lys Phe Phe Glu Gly Trp Tyr
                85                  90                  95

Phe Arg Val Ser Ile Pro Glu Lys Arg Glu Ser Phe Cys Phe Met Tyr
            100                 105                 110

Ser Val Glu Asn Pro Ala Phe Arg Gln Ser Leu Ser Pro Leu Glu Val
        115                 120                 125

Ala Leu Tyr Gly Pro Arg Phe Thr Gly Val Gly Ala Gln Ile Leu Gly
    130                 135                 140

Ala Asn Asp Lys Tyr Leu Cys Gln Tyr Glu Gln Asp Ser His Asn Phe
145                 150                 155                 160

Trp Gly Asp Arg His Glu Leu Val Leu Gly Asn Thr Phe Ser Ala Val
                165                 170                 175

Pro Gly Ala Lys Ala Pro Asn Lys Glu Val Pro Pro Glu Glu Phe Asn
            180                 185                 190

Arg Arg Val Ser Glu Gly Phe Gln Ala Thr Pro Phe Trp His Gln Gly
        195                 200                 205

His Ile Cys Asp Asp Gly Arg Thr Asp Tyr Ala Glu Thr Val Lys Ser
    210                 215                 220

Ala Arg Trp Glu Tyr Ser Thr Arg Pro Val Tyr Gly Trp Gly Asp Val
225                 230                 235                 240
```

```
Gly Ala Lys Gln Lys Ser Thr Ala Gly Trp Pro Ala Ala Phe Pro Val
                245                 250                 255

Phe Glu Pro His Trp Gln Ile Cys Met Ala Gly Gly Leu Ser Thr Gly
            260                 265                 270

Trp Ile Glu Trp Gly Gly Glu Arg Phe Glu Phe Arg Asp Ala Pro Ser
        275                 280                 285

Tyr Ser Glu Lys Asn Trp Gly Gly Gly Phe Pro Arg Lys Trp Phe Trp
    290                 295                 300

Val Gln Cys Asn Val Phe Glu Gly Ala Thr Gly Glu Val Ala Leu Thr
305                 310                 315                 320

Ala Gly Gly Gly Leu Arg Gln Leu Pro Gly Leu Thr Glu Thr Tyr Glu
                325                 330                 335

Asn Ala Ala Leu Val Cys Val His Tyr Asp Gly Lys Met Tyr Glu Phe
            340                 345                 350

Val Pro Trp Asn Gly Val Val Arg Trp Glu Met Ser Pro Trp Gly Tyr
        355                 360                 365

Trp Tyr Ile Thr Ala Glu Asn Glu Asn His Val Val Glu Leu Glu Ala
    370                 375                 380

Arg Thr Asn Glu Ala Gly Thr Pro Leu Arg Ala Pro Thr Thr Glu Val
385                 390                 395                 400

Gly Leu Ala Thr Ala Cys Arg Asp Ser Cys Tyr Gly Glu Leu Lys Leu
                405                 410                 415

Gln Ile Trp Glu Arg Leu Tyr Asp Gly Ser Lys Gly Lys Val Ile Leu
            420                 425                 430

Glu Thr Lys Ser Ser Met Ala Ala Val Glu Ile Gly Gly Gly Pro Trp
        435                 440                 445

Phe Gly Thr Trp Lys Gly Asp Thr Ser Asn Thr Pro Glu Leu Leu Lys
    450                 455                 460

Gln Ala Leu Gln Val Pro Leu Asp Leu Glu Ser Ala Leu Gly Leu Val
465                 470                 475                 480

Pro Phe Phe Lys Pro Pro Gly Leu
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<210> 111
<211> 246
<212> PRT
<213> Arabidopsis sp.

<400> 111

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 1               5                  10                  15

Thr Lys Leu His Val Asp Ser Val Thr Phe Val Pro Ser Val Lys Ser
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20 25 30

Pro Ala Ser Ser Asn Pro Leu Phe Leu Gly Gly Ala Gly Val Arg Gly
35 40 45

Leu Asp Ile Gln Gly Lys Phe Val Ile Phe Thr Val Ile Gly Val Tyr
50 55 60

Leu Glu Gly Asn Ala Val Pro Ser Leu Ser Val Lys Trp Lys Gly Lys
65 70 75 80

Thr Thr Glu Glu Leu Thr Glu Ser Ile Pro Phe Phe Arg Glu Ile Val
85 90 95

Thr Gly Ala Phe Glu Lys Phe Ile Lys Val Thr Met Lys Leu Pro Leu
100 105 110

Thr Gly Gln Gln Tyr Ser Glu Lys Val Thr Glu Asn Cys Val Ala Ile
115 120 125

Trp Lys Gln Leu Gly Leu Tyr Thr Asp Cys Glu Ala Lys Ala Val Glu
130 135 140

Lys Phe Leu Glu Ile Phe Lys Glu Glu Thr Phe Pro Pro Gly Ser Ser
145 150 155 160

Ile Leu Phe Ala Leu Ser Pro Thr Gly Ser Leu Thr Val Ala Phe Ser
165 170 175

Lys Asp Asp Ser Ile Pro Glu Thr Gly Ile Ala Val Ile Glu Asn Lys
180 185 190

Leu Leu Ala Glu Ala Val Leu Glu Ser Ile Ile Gly Lys Asn Gly Val
195 200 205

Ser Pro Gly Thr Arg Leu Ser Val Ala Glu Arg Leu Ser Gln Leu Met
210 215 220

Met Lys Asn Lys Asp Glu Lys Glu Val Ser Asp His Ser Leu Glu Glu
225 230 235 240

Lys Leu Ala Lys Glu Asn
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<210> 112
<211> 3115
<212> DNA
<213> Arabidopsis sp.

<400> 112

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aaacctgttt acgtcccgac gtctcccaat cgcgaactcc ggactcctca cagtgggtaa 360

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tggctcacca ttcgacgact acttttgaat ttgagttttt gaaaaatgca atttaacatc 600

agagagtttt ttttttatg gttgataact tattgtttaa cttttgaaaa atgcagatac 660

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tgaaagaaga ttatgaacgt ttgttatggt taacaatgat gcaggtgata ttagagacaa 2760

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tattatgtat gtatgatttt agttcgttcg gtccttgtgg taaatgatac gggccagtgt 3060

aaagtctagt tcaataaaag ccttgagtcg cataatttca atttcaaatt gcatc 3115

<210> 113
<211> 536
<212> DNA
<213> Arabidopsis sp.

<400> 113

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gtttgtcacc attggaagtg gctctatatg gacctagatt cactggtgtt ggagctcaga 480
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<210> 114
<211> 411
<212> PRT
<213> Arabidopsis sp.

<220>
<223> Peptide PIR: TO4448 shown in Figure 31

<400> 114

Pro Glu Lys Arg Glu Ser Phe Cys Phe Met Tyr Ser Val Glu Asn Pro
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Ala Phe Arg Gln Ser Leu Ser Pro Leu Glu Val Ala Leu Tyr Gly Pro
20 25 30

Arg Phe Thr Gly Val Gly Ala Gln Ile Leu Gly Ala Asn Asp Lys Tyr
35 40 45

Leu Cys Gln Tyr Glu Gln Asp Ser His Asn Phe Trp Gly Asp Arg His
50 55 60

Glu Leu Val Leu Gly Asn Thr Phe Ser Ala Val Pro Gly Ala Lys Ala
65 70 75 80

Pro Asn Lys Glu Val Pro Pro Glu Glu Phe Asn Arg Arg Val Ser Glu
85 90 95

Gly Phe Gln Ala Thr Pro Phe Trp His Gln Gly His Ile Cys Asp Asp
100 105 110

Gly Arg Thr Asp Tyr Ala Glu Thr Val Lys Ser Ala Arg Trp Glu Tyr
115 120 125

Ser Thr Arg Pro Val Tyr Gly Trp Gly Asp Val Gly Ala Lys Gln Lys
130 135 140

Ser Thr Ala Gly Trp Pro Ala Ala Phe Pro Val Phe Glu Pro His Trp
145 150 155 160

Gln Ile Cys Met Ala Gly Gly Leu Ser Thr Gly Trp Ile Glu Trp Gly
165 170 175

Gly Glu Arg Phe Glu Phe Arg Asp Ala Pro Ser Tyr Ser Glu Lys Asn
180 185 190

Trp Gly Gly Gly Phe Pro Arg Lys Trp Phe Trp Val Gln Cys Asn Val
195 200 205

Phe Glu Gly Ala Thr Gly Glu Val Ala Leu Thr Ala Gly Gly Gly Leu
210 215 220

Arg Gln Leu Pro Gly Leu Thr Glu Thr Tyr Glu Asn Ala Ala Leu Val
225 230 235 240

Cys Val His Tyr Asp Gly Lys Met Tyr Glu Phe Val Pro Trp Asn Gly
245 250 255

Val Val Arg Trp Glu Met Ser Pro Trp Gly Tyr Trp Tyr Ile Thr Ala
260 265 270

Glu Asn Glu Asn His Val Val Glu Leu Glu Ala Arg Thr Asn Glu Ala
275 280 285

Gly Thr Pro Leu Arg Ala Pro Thr Thr Glu Val Gly Leu Ala Thr Ala
290 295 300

Cys Arg Asp Ser Cys Tyr Gly Glu Leu Lys Leu Gln Ile Trp Glu Arg
305 310 315 320

Leu Tyr Asp Gly Ser Lys Gly Lys Leu Lys Val Leu Thr Asn Pro Lys
325 330 335

Ala Val Lys Glu Asp Tyr Glu Arg Leu Leu Trp Leu Thr Met Met Gln
340 345 350

Val Ile Leu Glu Thr Lys Ser Ser Met Ala Ala Val Glu Ile Gly Gly
355 360 365

Gly Pro Trp Phe Gly Thr Trp Lys Gly Asp Thr Ser Asn Thr Pro Glu
370 375 380

Leu Leu Lys Gln Ala Leu Gln Val Pro Leu Asp Leu Glu Ser Ala Leu
385 390 395 400

Gly Leu Val Pro Phe Phe Lys Pro Pro Gly Leu
405 410